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<110> Hannoufa, Abdelali
 Lydiate, Derek J.
 Gao, Ming-Jun

<120> REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS

<130> 270.78USWO

<140> US 10/516,753
 <141> 2004-12-03

<150> PCT/CA2003/000822
 <151> 2003-06-03

<150> US 60/387,088
 <151> 2002-06-06

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<170> PatentIn version 3.0

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Asp	Tyr	Pro	Met	Val	Ala	Pro	Ala	Tyr	Ala	Glu	Ala	Arg	Ser	Arg	Leu	115	120	125	
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Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
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His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Val
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 <223> EcoRV to ATG of GUS

 <400> 41
 gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata 60
 ctatataagg aagttcattt catttggaga gaacacgggg gactctagag gatccccggg 120
 tggtcagtcc cttatg 136

 <210> 42
 <211> 137
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> EcoRV to ATG of GUS

<400> 42
gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata 60
ctatataata tatttcaatt ttattgtaat ataacacggg ggactctaga ggatccccgg 120
gtggtcagtc ccttatg 137

<210> 43
<211> 237
<212> DNA
<213> Artificial Sequence

<220>
<223> EcoRV to ATG of GUS

<400> 43
gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca agacccttcc 60
tctatataat atatttcaat tttattgtaa tataacacgg gggactctag aggatcctat 120
atttcaattt tattgtaata tagctatatt tcaattttat tgtaatataa tcgatttcga 180
accgggggta ccgaattcct cgagtctaga ggatccccgg gtggtcagtc ccttatg 237

<210> 44
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for HDA19 A. thaliana, pDBLeu-HDA19

<400> 44
gcgtcgacga tggatactgg cggcaattcg c 31

<210> 45
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for HDA19 A. thaliana, pDBLeu-HDA19

<400> 45
aggcggccgc ttatgtttta ggaggaaacg cc 32

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for Gen5 Arabidopsis, GST-Gen5

<400> 46
 gcgtcgcacga tggactctca ctcttcccac c 31

<210> 47
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse primer for Gen5 Arabidopsis, GST-Gen5

<400> 47
 gcgcggccgc ctattgagat ttagcaccag a 31

<210> 48
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse primer forHDA19, GST-HDA19

<400> 48
 gcgcggccgc ttatgtttta ggaggaaacg c 31

<210> 49
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward primer for bnKCP1, 1-80, 1-160 (generation of mutants)

<400> 49
 gcaagcttat ggcaggagga ggaccaact 29

<210> 50
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse primer for bnKCP1 1-160 (generation of mutants)

<400> 50
 cgctcgagct cctcctcatc attgtcttc 29

<210> 51
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse primer for bnKCP1 1-80 (generation of mutants)

<400> 51
cgctcgagat gaacaggcaa aagaggcat 29

<210> 52
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for bnKCP1 (generation of mutants)

<400> 52
cgctcgagct catcttcttc ttcttcttc 29

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for bnKCP1, 1-80 and 1-160 (in vivo assay and transactivation assay)

<400> 53
gcgtcgacga tggcaggagg aggaccaact 30

<210> 54
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for bnKCP1

<400> 54
gcgcggccgc ctcatcttct tcttcttct c 31

<210> 55
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for bnKCP1

<400> 55
gcgcggccgc atgaacaggc aaaagaggca t 31

<210> 56
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for bnKCP1

<400> 56
 gcgcggccgc ctctctctca tcattgtctt c 31

<210> 57
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward primer for bnKCP1G188

<400> 57
 gatgttcttg cgaggagacc aggattcaag aacagagcat tgaag 45

<210> 58
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse primer for bnKCP1G188

<400> 58
 cttcaatgct ctgttcttga atcctgggtct cctcgcaaga acatc 45

<210> 59
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward primer for bnKCP1 81-215

<400> 59
 gcgtcgacgc tagggttggc ttcattgaga 30

<210> 60
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward primer for entire encoding region of bnKCP1

<400> 60
 gcgaattcat ggcaggagga ggaccaact 29

<210> 61
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse primer for entire coding region of bnKCP1

<400> 61
 cggagctcct catctttcttc ttctttcttc

29

<210> 62
 <211> 7
 <212> PRT
 <213> Brassica Napus

<220>
 <223> pat7 NLS

<400> 62
 Pro Leu Asn Lys Lys Arg Arg
 1 5

<210> 63
 <211> 143
 <212> PRT
 <213> Rhizobium Elti

<220>
 <223> ROSR (ROS repressor)

<400> 63
 Met Thr Asp Met Ala Thr Gly Asn Ala Pro Glu Leu Leu Val Glu Leu
 1 5 10 15
 Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
 20 25 30
 Ser Asp Leu Ala Asn Leu Ile Ser Asp Val His Ser Ala Leu Ser Asn
 35 40 45
 Thr Ser Val Pro Gln Pro Ala Ala Ala Val Val Glu Lys Gln Lys Pro
 50 55 60
 Ala Val Ser Val Arg Lys Ser Val Gln Asp Glu Gln Ile Thr Cys Leu
 65 70 75 80
 Glu Cys Gly Gly Asn Phe Lys Ser Leu Lys Arg His Leu Met Thr His
 85 90 95
 His Ser Leu Ser Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Thr
 100 105 110
 Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
 115 120 125
 Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Gly Arg Gly
 130 135 140

<210> 64
 <211> 142
 <212> PRT

<213> Agrobacterium Radiobacter

<220>

<223> ROSAR (ROS repressor)

<400> 64

Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu
1 5 10 15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
20 25 30

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly
35 40 45

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro
50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu
65 70 75 80

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
85 90 95

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Gln Val
100 105 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg
130 135 140

<210> 65

<211> 143

<212> PRT

<213> Rhizobium Melilotti

<220>

<223> MucR (ROS repressor)

<400> 65

Met Thr Glu Thr Ser Leu Gly Thr Ser Asn Glu Leu Leu Val Glu Leu
1 5 10 15

Thr Ala Glu Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
20 25 30

Ala Glu Leu Pro Thr Leu Ile Ala Asp Val His Ser Ala Leu Asn Asn
35 40 45

Thr Thr Ala Pro Ala Pro Val Val Val Pro Val Glu Lys Pro Lys Pro
50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp Gln Ile Thr Cys Leu
65 70 75 80

Glu Cys Gly Gly Thr Phe Lys Ser Leu Lys Arg His Leu Met Thr His
 85 90 95
 His Asn Leu Ser Pro Glu Glu Tyr Arg Asp Lys Trp Asp Leu Pro Ala
 100 105 110
 Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
 115 120 125
 Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Arg Gly Lys
 130 135 140

<210> 66
 <211> 10
 <212> DNA
 <213> Agrobacterium Tumefaciens

<220>
 <223> VirC/VirD DNA binding site seq (1)

<400> 66
 tatatttcaa 10

<210> 67
 <211> 10
 <212> DNA
 <213> Agrobacterium Tumefaciens

<220>
 <223> VirC/VirD DNA binding site seq (2)

<400> 67
 tatattacaa 10

<210> 68
 <211> 10
 <212> DNA
 <213> Agrobacterium Tumefaciens

<220>
 <223> ipt DNA binding site seq (1)

<400> 68
 tataattaataa 10

<210> 69
 <211> 10
 <212> DNA
 <213> Agrobacterium Tumefaciens

<220>
 <223> ipt DNA binding site seq (2)

<400> 69
 aatgcgacag 10

<210> 70
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> consensus DNA binding site seq

<400> 70
 tatahtttcaa

10

<210> 71
 <211> 215
 <212> PRT
 <213> Brassica Napus

<220>
 <223> bnKCP

<400> 71

Met Ala Gly Gly Gly Pro Thr Phe Ser Ile Glu Leu Ser Ala Tyr Gly
 1 5 10 15
 Ser Asp Leu Pro Thr Asp Lys Ala Ser Gly Asp Ile Pro Asn Glu Glu
 20 25 30
 Gly Ser Gly Leu Ser Arg Val Gly Ser Gly Ile Trp Ser Gly Arg Thr
 35 40 45
 Val Asp Tyr Ser Ser Glu Ser Ser Ser Ser Ile Gly Thr Pro Gly Asp
 50 55 60
 Ser Glu Glu Glu Asp Glu Glu Ser Glu Glu Asp Asn Asp Glu Glu Glu
 65 70 75 80
 Leu Gly Leu Ala Ser Leu Arg Ser Leu Glu Asp Ser Leu Pro Ser Lys
 85 90 95
 Gly Leu Ser Ser His Tyr Lys Gly Lys Ser Lys Ser Phe Gly Asn Leu
 100 105 110
 Gly Glu Ile Gly Ser Val Lys Glu Val Pro Lys Gln Glu Asn Pro Leu
 115 120 125
 Asn Lys Lys Arg Arg Leu Gln Ile Tyr Asn Lys Leu Ala Arg Lys Ser
 130 135 140
 Phe Tyr Ser Trp Gln Asn Pro Lys Ser Met Pro Leu Leu Pro Val His
 145 150 155 160
 Glu Asp Asn Asp Asp Glu Glu Gly Asp Asp Gly Asp Leu Ser Asp Glu
 165 170 175
 Glu Arg Gly Gly Asp Val Leu Ala Arg Arg Pro Ser Phe Lys Asn Arg
 180 185 190
 Ala Leu Lys Ser Met Ser Cys Phe Ala Leu Ser Asp Leu Gln Glu Glu

<210> 73
 <211> 214
 <212> PRT
 <213> Arabidopsis

<220>
 <223> atKCL1

<400> 73

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Met Glu Val Leu Val Gly Ser Thr Phe Arg Asp Arg Ser Ser Val Thr
1          5          10          15

Thr His Asp Gln Ala Val Pro Ala Ser Leu Ser Ser Arg Ile Gly Leu
          20          25          30

Arg Arg Cys Gly Arg Ser Pro Pro Pro Glu Ser Ser Ser Ser Val Gly
          35          40          45

Glu Thr Ser Glu Asn Glu Glu Asp Glu Asp Asp Ala Val Ser Ser Ser
50          55          60

Gln Gly Arg Trp Leu Asn Ser Phe Ser Ser Ser Leu Glu Asp Ser Leu
65          70          75          80

Pro Ile Lys Arg Gly Leu Ser Asn His Tyr Ile Gly Lys Ser Lys Ser
          85          90          95

Phe Gly Asn Leu Met Glu Ala Ser Asn Thr Asn Asp Leu Val Lys Val
          100          105          110

Glu Ser Pro Leu Asn Lys Arg Arg Arg Leu Leu Ile Ala Asn Lys Leu
          115          120          125

Arg Arg Arg Ser Ser Leu Ser Ser Phe Ser Ile Tyr Thr Lys Ile Asn
          130          135          140

Pro Asn Ser Met Pro Leu Leu Ala Leu Gln Glu Ser Asp Asn Glu Asp
145          150          155          160

His Lys Leu Asn Asp Asp Asp Asp Asp Asp Asp Ser Ser Ser Asp Asp
          165          170          175

Glu Thr Ser Lys Leu Lys Glu Lys Arg Met Lys Met Thr Asn His Arg
          180          185          190

Asp Phe Met Val Pro Gln Thr Lys Ser Cys Phe Ser Leu Thr Ser Phe
          195          200          205

Gln Asp Asp Asp Asp Arg
          210

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<210> 74
 <211> 221
 <212> PRT
 <213> Arabidopsis

<220>
<223> atKCL2

<400> 74

Met Val Gly Ser Ser Phe Gly Ile Gly Met Ala Ala Tyr Val Arg Asp
1 5 10 15
His Arg Gly Val Ser Ala Gln Asp Lys Ala Val Gln Thr Ala Leu Phe
20 25 30
Leu Ala Asp Glu Ser Gly Arg Gly Gly Ser Gln Ile Gly Ile Gly Leu
35 40 45
Arg Met Ser Asn Asn Asn Asn Lys Ser Pro Glu Glu Ser Ser Asp Ser
50 55 60
Ser Ser Ser Ile Gly Glu Ser Ser Glu Asn Glu Glu Glu Glu Glu
65 70 75 80
Asp Asp Ala Val Ser Cys Gln Arg Gly Thr Leu Asp Ser Phe Ser Ser
85 90 95
Ser Leu Glu Asp Ser Leu Pro Ile Lys Arg Gly Leu Ser Asn His Tyr
100 105 110
Val Gly Lys Ser Lys Ser Phe Gly Asn Leu Met Glu Ala Ala Ser Lys
115 120 125
Ala Lys Asp Leu Glu Lys Val Glu Asn Pro Phe Asn Lys Arg Arg Arg
130 135 140
Leu Val Ile Ala Asn Lys Leu Arg Arg Arg Gly Arg Ser Ile Thr Tyr
145 150 155 160
Glu Glu Asp His His Ile His Asn Asp Asp Tyr Glu Asp Asp Asp Gly
165 170 175
Asp Gly Asp Asp His Arg Lys Ile Met Met Met Met Lys Asn Lys Lys
180 185 190
Glu Leu Met Ala Gln Thr Arg Ser Cys Phe Cys Leu Ser Ser Leu Gln
195 200 205
Glu Glu Asp Asp Gly Asp Gly Asp Asp Asp Glu Asp Glu
210 215 220

<210> 75
<211> 42
<212> PRT
<213> Brassica Napus

<220>
<223> bnKCP Fragment

<400> 75

Gly Asp Asp Gly Asp Leu Ser Asp Glu Glu Arg Gly Gly Asp Val Leu
1 5 10 15

Ala Arg Arg Pro Ser Phe Lys Asn Arg Ala Leu Lys Ser Met Ser Cys
20 25 30

Phe Ala Leu Ser Asp Leu Gln Glu Glu Glu
35 40

<210> 76
<211> 42
<212> PRT
<213> Human

<220>
<223> ATF-1

<400> 76

Asp Ser Ser Asp Ser Ile Gly Ser Ser Gln Gln Ala His Gly Ile Leu
1 5 10 15

Ala Arg Arg Pro Ser Tyr Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu
20 25 30

Asp Thr Arg Gly Arg Lys Gly Asp Gly Glu
35 40

<210> 77
<211> 42
<212> PRT
<213> Human

<220>
<223> hyCREB

<400> 77

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
20 25 30

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu
35 40

<210> 78
<211> 42
<212> PRT
<213> Human

<220>
<223> CREB

<400> 78

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
20 25 30

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu
35 40

<210> 79
<211> 42
<212> PRT
<213> Mouse

<220>
<223> CREM

<400> 79

Ser Ala Asp Ser Glu Val Ile Asp Ser His Lys Arg Arg Glu Ile Leu
1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Glu Leu Ser Ser Asp
20 25 30

Val Pro Gly Ile Pro Lys Ile Glu Glu Glu
35 40

<210> 80
<211> 42
<212> PRT
<213> Human

<220>
<223> cCREM

<400> 80

Ala Glu Ser Glu Gly Val Ile Asp Ser His Lys Arg Arg Glu Ile Leu
1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Glu Leu Ser Ser Asp
20 25 30

Val Pro Gly Val Pro Lys Ile Glu Glu Glu
35 40

<210> 81
<211> 461
<212> PRT
<213> Brassica Napus

<220>
<223> BNSCL1

<400> 81

Met Lys Leu Gln Ala Ser Ser Pro Gln Asp Asn Gln Pro Ser Asn Thr
1 5 10 15

Thr	Asn	Asn	Ser	Thr	Asp	Ser	Asn	His	Leu	Ser	Met	Asp	Glu	His	Ala		
			20					25					30				
Met	Arg	Ser	Met	Asp	Trp	Asp	Ser	Ile	Met	Lys	Glu	Leu	Glu	Val	Asp		
		35					40					45					
Asp	Asp	Ser	Ala	Pro	Tyr	Gln	Leu	Gln	Pro	Ser	Ser	Phe	Asn	Leu	Pro		
	50					55					60						
Val	Phe	Pro	Asp	Ile	Asp	Ser	Ser	Asp	Val	Tyr	Pro	Gly	Pro	Asn	Gln		
65					70					75					80		
Ile	Thr	Gly	Tyr	Gly	Phe	Asn	Ser	Leu	Asp	Ser	Val	Asp	Asn	Gly	Gly		
				85					90					95			
Phe	Asp	Tyr	Ile	Glu	Asp	Leu	Ile	Arg	Val	Val	Asp	Cys	Ile	Glu	Ser		
			100					105					110				
Asp	Glu	Leu	His	Leu	Ala	His	Val	Val	Leu	Ser	Gln	Leu	Asn	Gln	Arg		
		115					120					125					
Leu	Gln	Thr	Ser	Ala	Gly	Arg	Pro	Leu	Gln	Arg	Ala	Ala	Phe	Tyr	Phe		
	130					135					140						
Lys	Glu	Ala	Leu	Gly	Ser	Leu	Leu	Thr	Gly	Thr	Asn	Arg	Asn	Gln	Leu		
145					150					155					160		
Phe	Ser	Trp	Ser	Asp	Ile	Val	Gln	Lys	Ile	Arg	Ala	Ile	Lys	Glu	Phe		
				165					170					175			
Ser	Gly	Ile	Ser	Pro	Ile	Pro	Leu	Phe	Ser	His	Phe	Thr	Ala	Asn	Gln		
			180					185						190			
Ala	Ile	Leu	Asp	Ser	Leu	Ser	Ser	Gln	Ser	Ser	Ser	Pro	Phe	Val	His		
		195					200					205					
Val	Val	Asp	Phe	Glu	Ile	Gly	Phe	Gly	Gly	Gln	Tyr	Ala	Ser	Leu	Met		
	210					215					220						
Arg	Glu	Ile	Ala	Glu	Lys	Ser	Ala	Asn	Gly	Gly	Phe	Leu	Arg	Val	Thr		
225					230					235					240		
Ala	Val	Val	Ala	Glu	Asp	Cys	Ala	Val	Glu	Thr	Arg	Leu	Val	Lys	Glu		
				245					250					255			
Asn	Leu	Thr	Gln	Phe	Ala	Ala	Glu	Met	Lys	Ile	Arg	Phe	Gln	Ile	Glu		
			260					265					270				
Phe	Val	Leu	Met	Lys	Thr	Phe	Glu	Ile	Leu	Ser	Phe	Lys	Ala	Ile	Arg		
		275					280					285					
Phe	Val	Asp	Gly	Glu	Arg	Thr	Val	Val	Leu	Ile	Ser	Pro	Ala	Ile	Phe		
	290					295					300						
Arg	Arg	Val	Ile	Gly	Ile	Ala	Glu	Phe	Val	Asn	Asn	Leu	Gly	Arg	Val		
305					310					315					320		
Ser	Pro	Asn	Val	Val	Val	Phe	Val	Asp	Ser	Glu	Gly	Cys	Thr	Glu	Thr		
				325					330					335			

Ala Gly Ser Gly Ser Phe Arg Arg Glu Phe Val Ser Ala Phe Glu Phe
 340 345 350
 Tyr Thr Met Val Leu Glu Ser Leu Asp Ala Ala Ala Pro Pro Gly Asp
 355 360 365
 Leu Val Lys Lys Ile Val Glu Thr Phe Leu Leu Arg Pro Lys Ile Ser
 370 375 380
 Ala Ala Val Glu Thr Ala Ala Asn Arg Arg Ser Ala Gly Gln Met Thr
 385 390 395 400
 Trp Arg Glu Met Leu Cys Ala Ala Gly Met Arg Pro Val Gln Leu Ser
 405 410 415
 Gln Phe Ala Asp Phe Gln Ala Glu Cys Leu Leu Glu Lys Ala Gln Val
 420 425 430
 Arg Gly Phe His Val Ala Lys Arg Gln Gly Glu Leu Val Leu Cys Trp
 435 440 445
 His Gly Arg Ala Leu Val Ala Thr Ser Ala Trp Arg Phe
 450 455 460

<210> 82
 <211> 486
 <212> PRT
 <213> Arabidopsis

<220>
 <223> atSCL15

<400> 82

Met Lys Ile Pro Ala Ser Ser Pro Gln Asp Thr Thr Asn Asn Asn Asn
 1 5 10 15
 Asn Thr Asn Ser Thr Asp Ser Asn His Leu Ser Met Asp Glu His Val
 20 25 30
 Met Arg Ser Met Asp Trp Asp Ser Ile Met Lys Glu Leu Glu Leu Asp
 35 40 45
 Asp Asp Ser Ala Pro Asn Ser Leu Lys Thr Gly Phe Thr Thr Thr Thr
 50 55 60
 Thr Asp Ser Thr Ile Leu Pro Leu Tyr Ala Val Asp Ser Asn Leu Pro
 65 70 75 80
 Gly Phe Pro Asp Gln Ile Gln Pro Ser Asp Phe Glu Ser Ser Ser Asp
 85 90 95
 Val Tyr Pro Gly Gln Asn Gln Thr Thr Gly Tyr Gly Phe Asn Ser Leu
 100 105 110
 Asp Ser Val Asp Asn Gly Gly Phe Asp Phe Ile Glu Asp Leu Ile Arg
 115 120 125

Glu Cys Leu Leu Glu Lys Ala Gln Val Arg Gly Phe His Val Ala Lys
 450 455 460

Arg Gln Gly Glu Leu Val Leu Cys Trp His Gly Arg Ala Leu Val Ala
 465 470 475 480

Thr Ser Ala Trp Arg Phe
 485

<210> 83
 <211> 536
 <212> PRT
 <213> Lycopersicon Esculentum

<220>
 <223> lsSCR

<400> 83

Met Lys Val Pro Phe Ser Thr Asn Asp Asn Val Ser Ser Lys Pro Leu
 1 5 10 15

Val Asn Ser Asn Asn Ser Phe Thr Phe Pro Ala Ala Thr Asn Gly Ser
 20 25 30

Asn Leu Cys Tyr Glu Pro Lys Ser Val Leu Glu Leu Arg Arg Ser Pro
 35 40 45

Ser Pro Ile Val Asp Lys Gln Ile Ile Thr Thr Asn Pro Asp Leu Ser
 50 55 60

Ala Leu Cys Gly Gly Glu Asp Pro Leu Gln Leu Gly Asp His Val Leu
 65 70 75 80

Ser Asn Phe Glu Asp Trp Asp Ser Leu Met Arg Glu Leu Gly Leu His
 85 90 95

Asp Asp Ser Ala Ser Leu Ser Lys Thr Asn Pro Leu Thr His Ser Glu
 100 105 110

Ser Leu Thr Gln Phe His Asn Leu Ser Glu Phe Ser Ala Glu Ser Asn
 115 120 125

Gln Phe Pro Ser Pro Asp Phe Ser Phe Ser Asp Thr Asn Phe Pro Gln
 130 135 140

Gln Phe Pro Thr Val Asn Gln Ala Ser Phe Ile Asn Ala Leu Asp Leu
 145 150 155 160

Ser Gly Asp Ile His Gln Asn Trp Ser Val Gly Phe Asp Tyr Val Asp
 165 170 175

Glu Leu Ile Arg Phe Ala Glu Cys Phe Glu Thr Asn Ala Phe Gln Leu
 180 185 190

Ala His Val Ile Leu Ala Arg Leu Asn Gln Arg Leu Arg Ser Ala Ala
 195 200 205

Gly Lys Pro Leu Gln Arg Ala Ala Phe Tyr Phe Lys Glu Ala Leu Gln

210	215	220
Ala Gln Leu Ala Gly Ser Ala Arg Gln Thr Arg Ser Ser Ser Ser Ser		
225	230	235 240
Asp Val Ile Gln Thr Ile Lys Ser Tyr Lys Ile Leu Ser Asn Ile Ser		
	245	250 255
Pro Ile Pro Met Phe Ser Ser Phe Thr Ala Asn Gln Ala Val Leu Glu		
	260	265 270
Ala Val Asp Gly Ser Met Leu Val His Val Ile Asp Phe Asp Ile Gly		
	275	280 285
Leu Gly Gly His Trp Ala Ser Phe Met Lys Glu Leu Ala Asp Lys Ala		
	290	295 300
Glu Cys Arg Lys Ala Asn Ala Pro Ile Leu Arg Ile Thr Ala Leu Val		
305	310	315 320
Pro Glu Glu Tyr Ala Val Glu Ser Arg Leu Ile Arg Glu Asn Leu Thr		
	325	330 335
Gln Phe Ala Arg Glu Leu Asn Ile Gly Phe Glu Ile Asp Phe Val Leu		
	340	345 350
Ile Arg Thr Phe Glu Leu Leu Ser Phe Lys Ala Ile Lys Phe Met Glu		
	355	360 365
Gly Glu Lys Thr Ala Val Leu Leu Ser Pro Ala Ile Phe Arg Arg Val		
	370	375 380
Gly Ser Gly Phe Val Asn Glu Leu Arg Arg Ile Ser Pro Asn Val Val		
385	390	395 400
Val His Val Asp Ser Glu Gly Leu Met Gly Tyr Gly Ala Met Ser Phe		
	405	410 415
Arg Gln Thr Val Ile Asp Gly Leu Glu Phe Tyr Ser Thr Leu Leu Glu		
	420	425 430
Ser Leu Glu Ala Ala Asn Ile Gly Gly Gly Asn Cys Gly Asp Trp Met		
	435	440 445
Arg Lys Ile Glu Asn Phe Val Leu Phe Pro Lys Ile Val Asp Met Ile		
	450	455 460
Gly Ala Val Gly Arg Arg Gly Gly Gly Gly Ser Trp Arg Asp Ala Met		
465	470	475 480
Val Asp Ala Gly Phe Arg Pro Val Gly Leu Ser Gln Phe Ala Asp Phe		
	485	490 495
Gln Ala Asp Cys Leu Leu Gly Arg Val Gln Val Arg Gly Phe His Val		
	500	505 510
Ala Lys Arg Gln Ala Glu Met Leu Leu Cys Trp His Asp Arg Ala Leu		
	515	520 525
Val Ala Thr Ser Ala Trp Arg Cys		

<210> 84
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BnSCL1 sense primer

<400> 84
 gatggacgaa catgccatgc gttcca

26

<210> 85
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BnSCL1 anti-sense primer

<400> 85
 cgctcggatc ttctgaacaa t

21

<210> 86
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BnIAA1 sense primer

<400> 86
 ccacgcgtcc ggtacgatga t

21

<210> 87
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BnIAA1 anti-sense primer

<400> 87
 gaagttgaga aatggtttat ga

22

<210> 88
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BnIAA12 sense primer

<400> 88

acgctggtgc ttctcctcct c 21

<210> 89
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BNIAA12 anti-sense primer

<400> 89
 aaaacccatt agaagaacca agaa 24

<210> 90
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
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 and BnSCL1 1-145 for pET-28b vector

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Leu Gly Ser Leu Leu
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